FIG. 1B

P-Selectin Binding to COS M6 Cells Expressing PSGL-1-NH2 Gross Deletion Mutants

PSGL-1

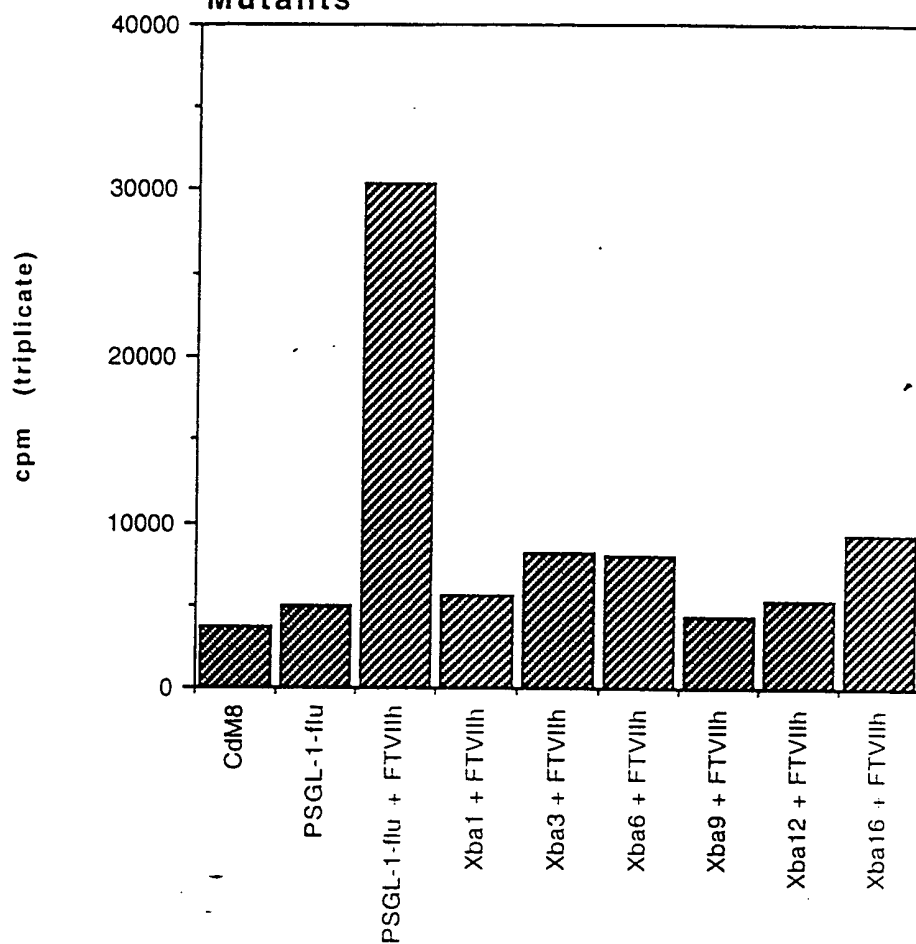(ATEAQTTPPA)

TM

PSGL-1-NH$_2$/CD43-COOH

(ATEAQTTPPA)

TM
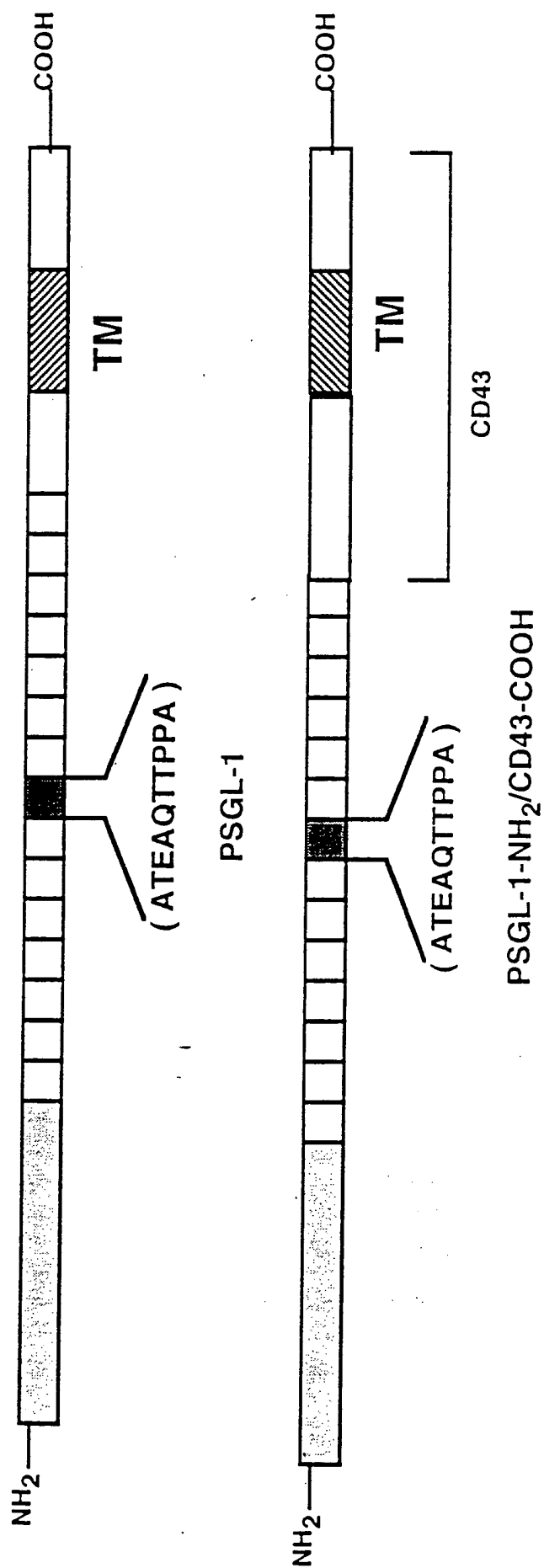
CD43

P-Selectin Binding to COS Cells Expressing
Chimeric PSGL-1/CD43 Constructs

NH₂

TM

(ATEAQTTPPA)

PSGL-1

NH₂

TM

(MATNSLETSTGTSGPPVT)

PSGL-1-NH₂/CD43 "repeats"

NH₂

High Serine/Threonine Content

TM

PSGL-1-NH₂/CD34-COOH

NH₂

High Serine/Threonine Content

TM

PSGL-1-NH₂/Glycam/CD7-COOH
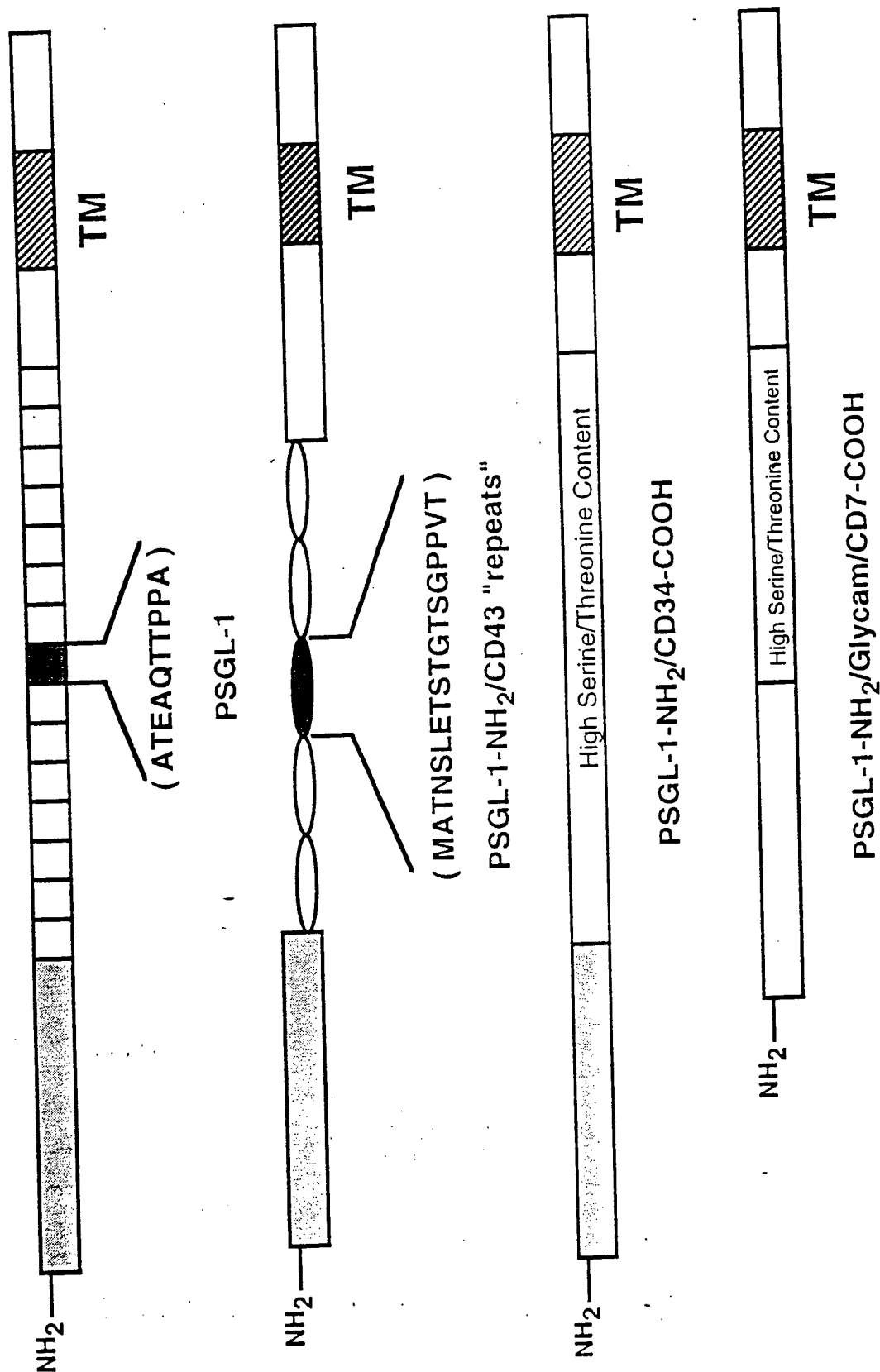
FIG. 3B

P-Selectin Binding to COS M6 Cells Expressing PSGL-1-NH2/Mucin Chimeric Constructs

1R1

2R1

3R1

4R1

5R1

6R1

7R1

8R1

16R1

TM

(ATEAQTTPPA)
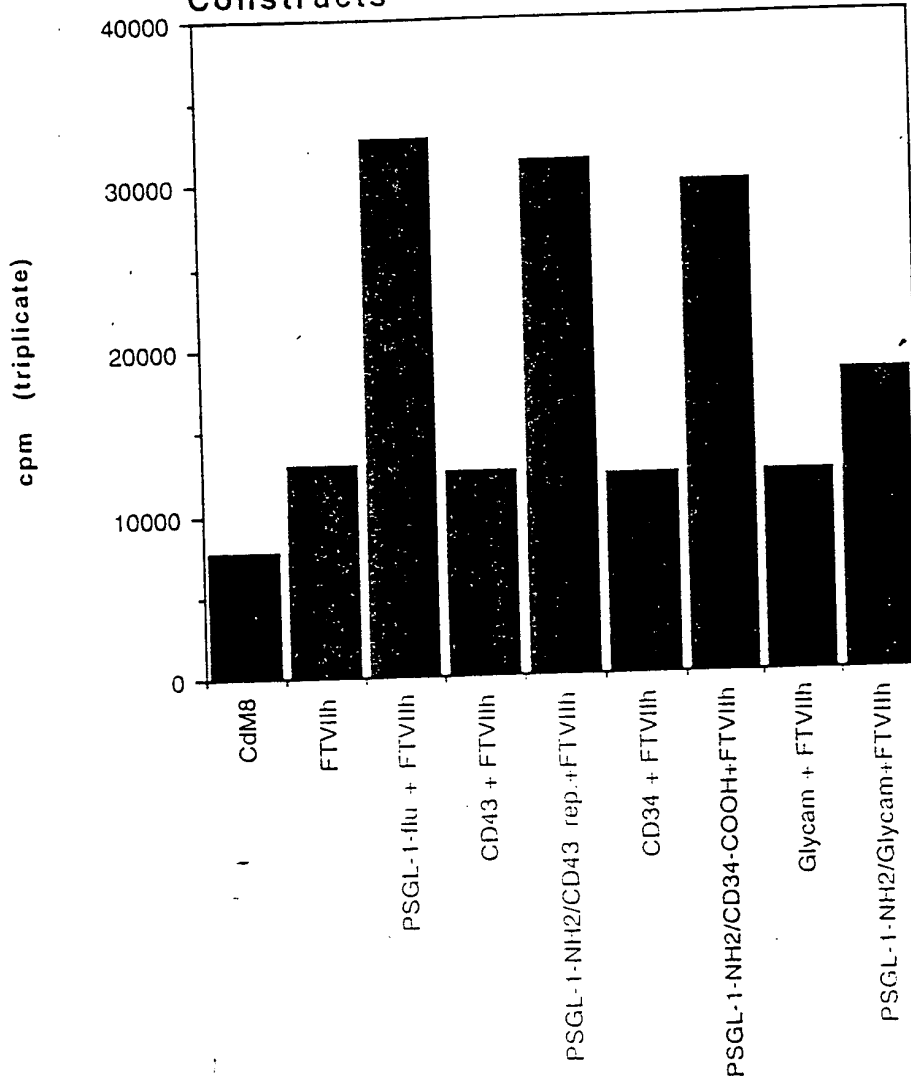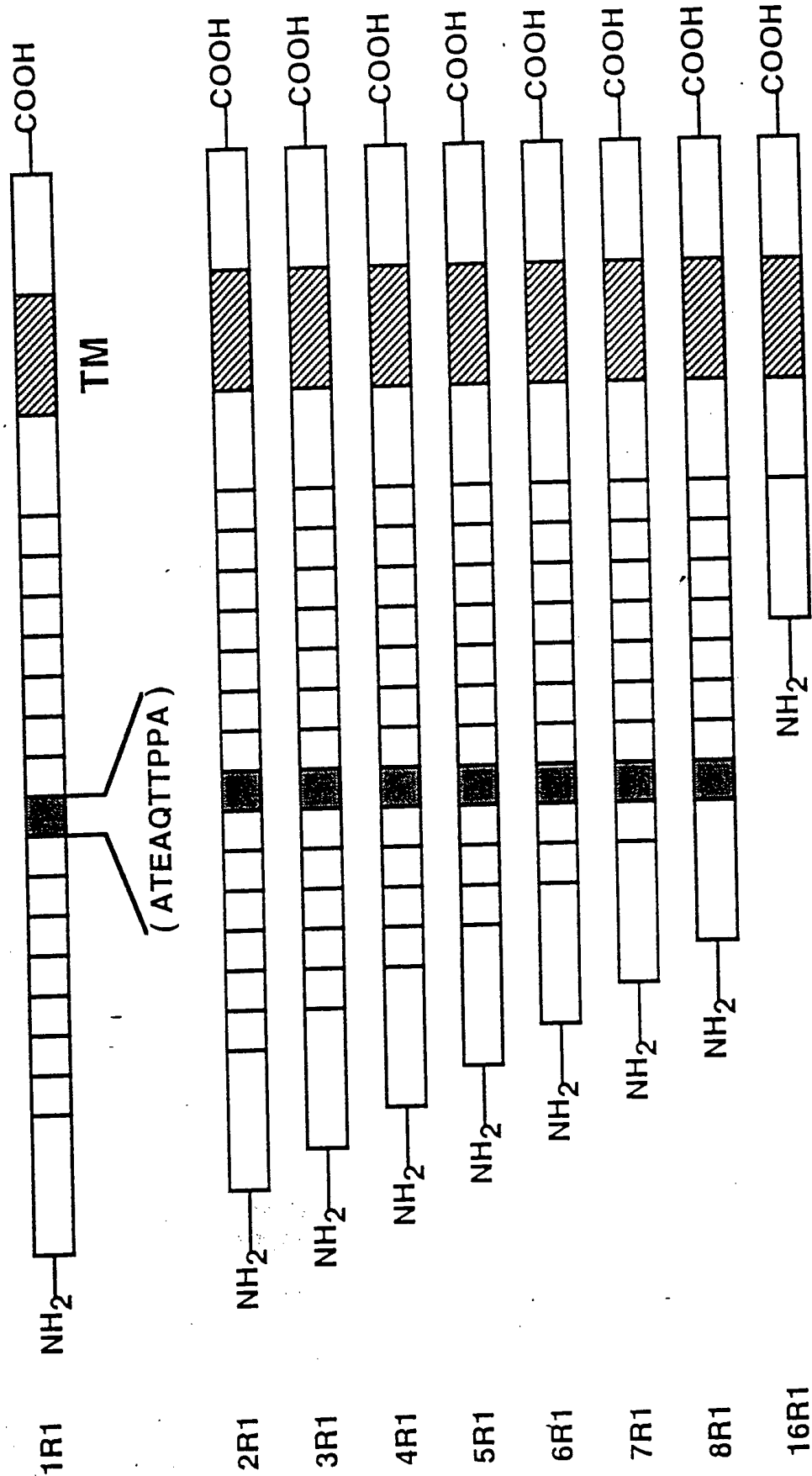
FIG. 4B

P-Selectin Binding to COS M6 Cells
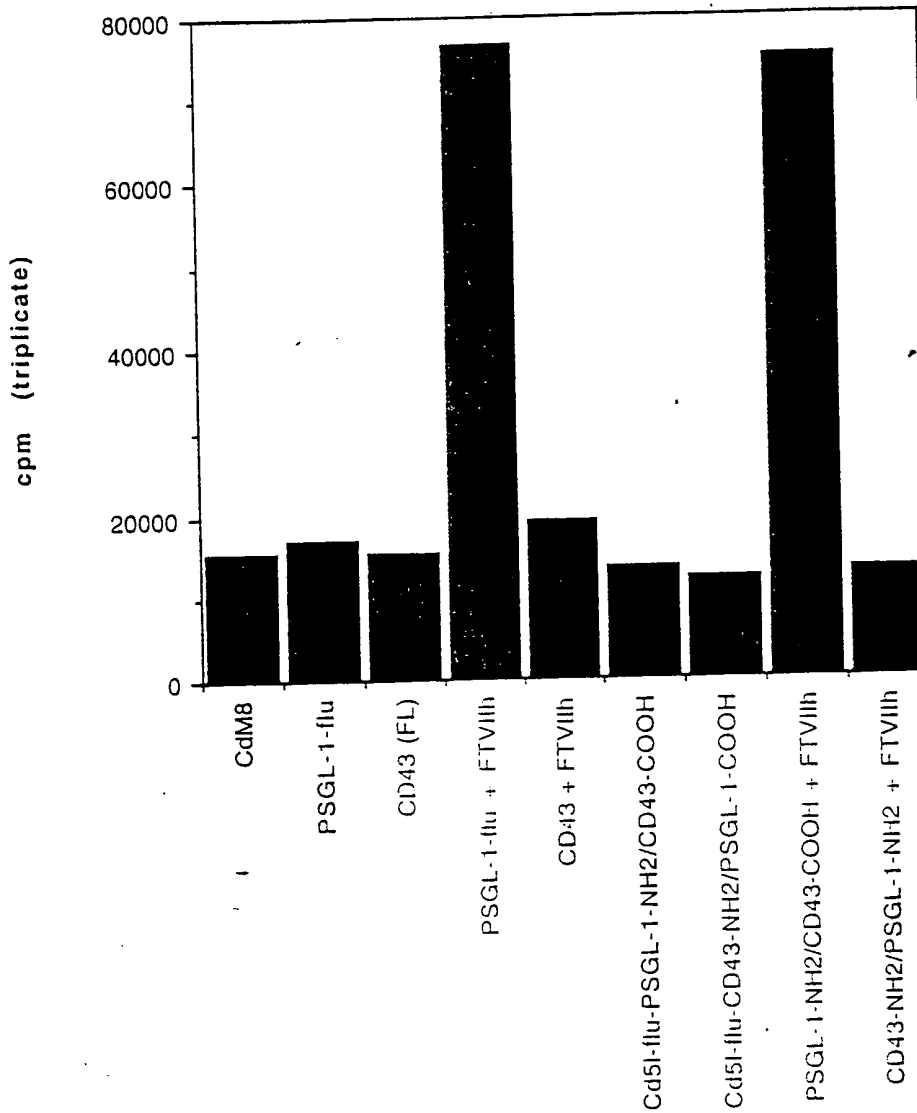Expressing PSGL-1 Internal Deletion
Mutants

FIG. 5

A B C D E F G

200kD →

92kD →

67kD →

46kD →
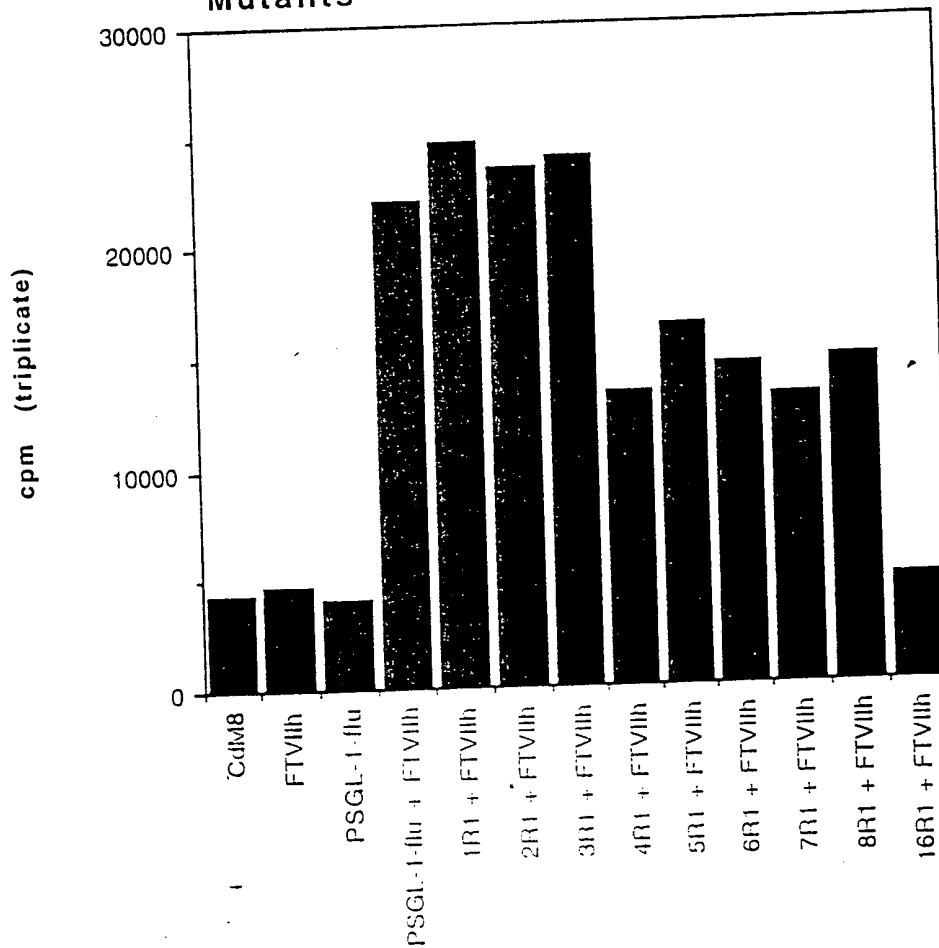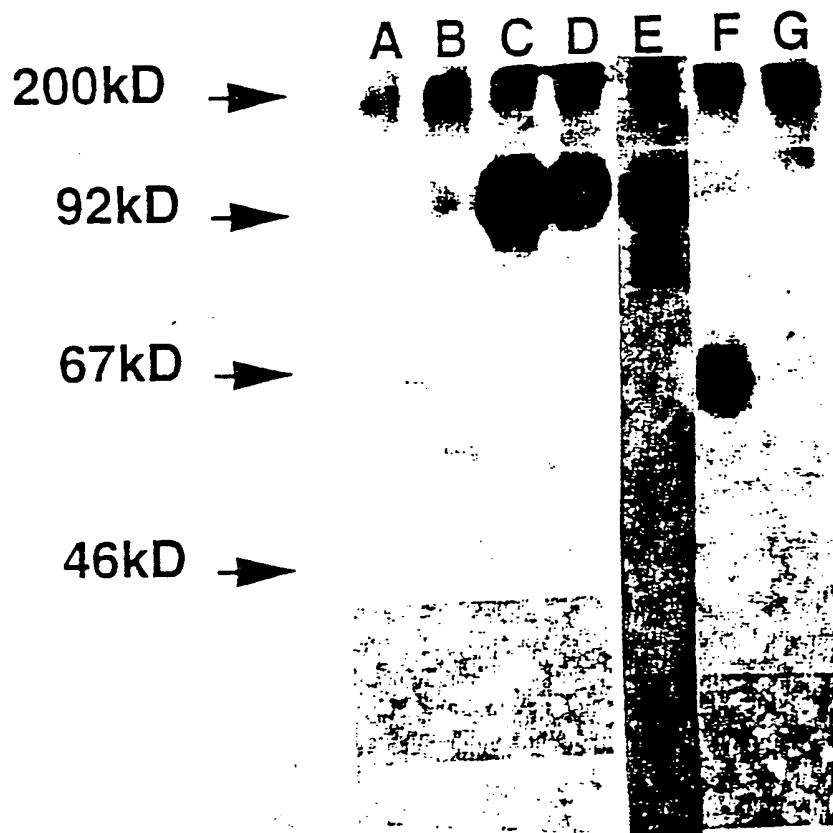
FIG. 6A

P-Selectin Binding to COS M6 Cells Expressing PSGL-1/FTVIIh w and w/0 NaClO3

FIG. 6B

E-Selectin Binding to COS M6 Cells Expressing PSGL-1/FTVIIh w and w/o NaClO3

FIG. 7

A B C D

200kD →

92kD →

67kD →

46kD →

Q19

R38   E58

QLWDTWADEAEKALGPLLARDRRQATEYEYLDYDFLPETEPP

P78   A98

PEMLRNSTDTTPLTGPGTPESTTVEPAARRSTGLDAGGAVTE

A108

LTTELANMGNLSTDSA
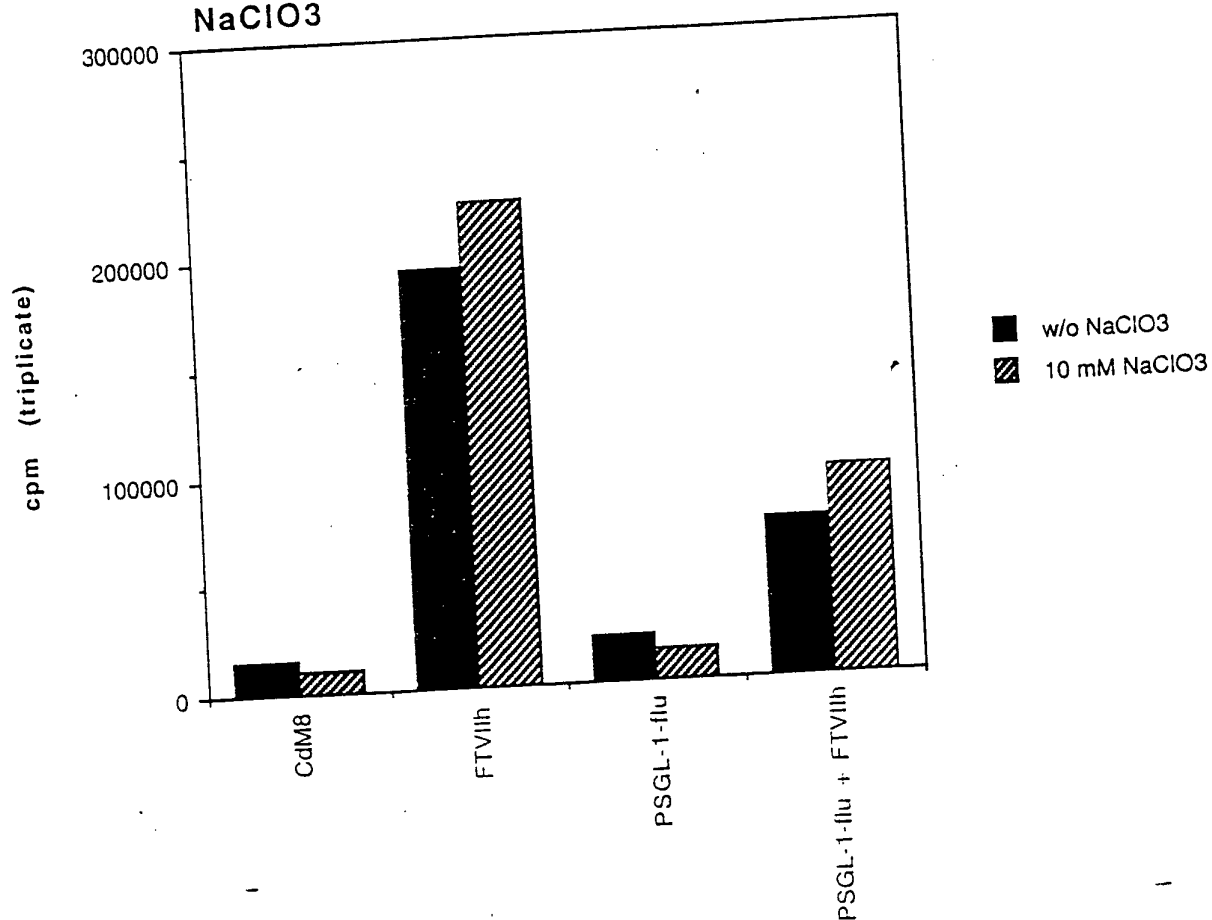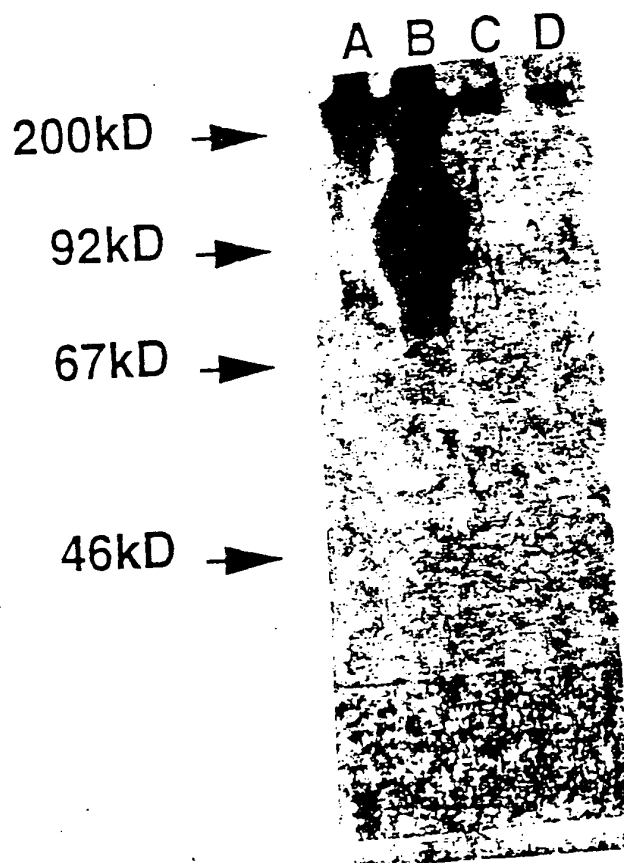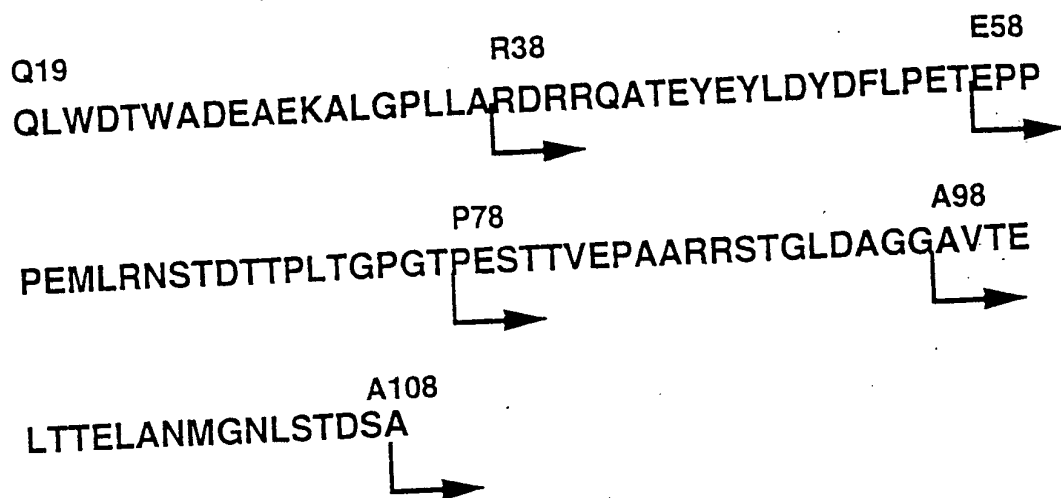
FIG. 8B

P-Selectin Binding to COS M6 Cells Expressing PSGL-1-NH2 Terminus Deletion Mutants
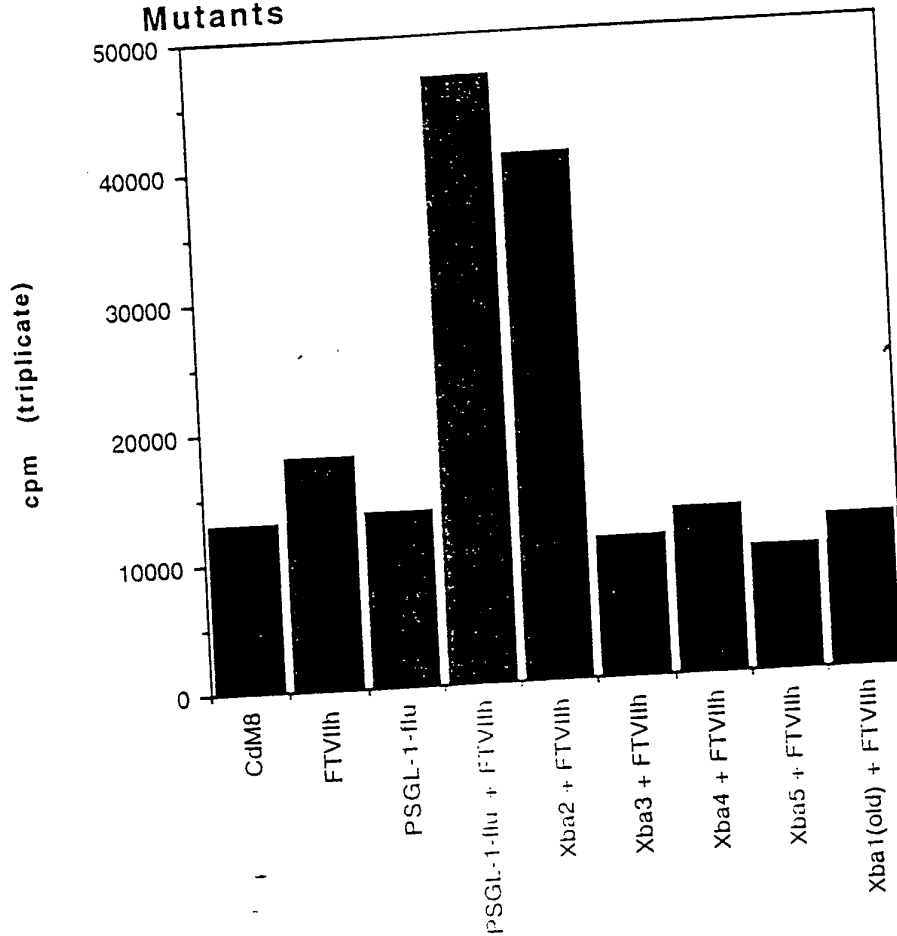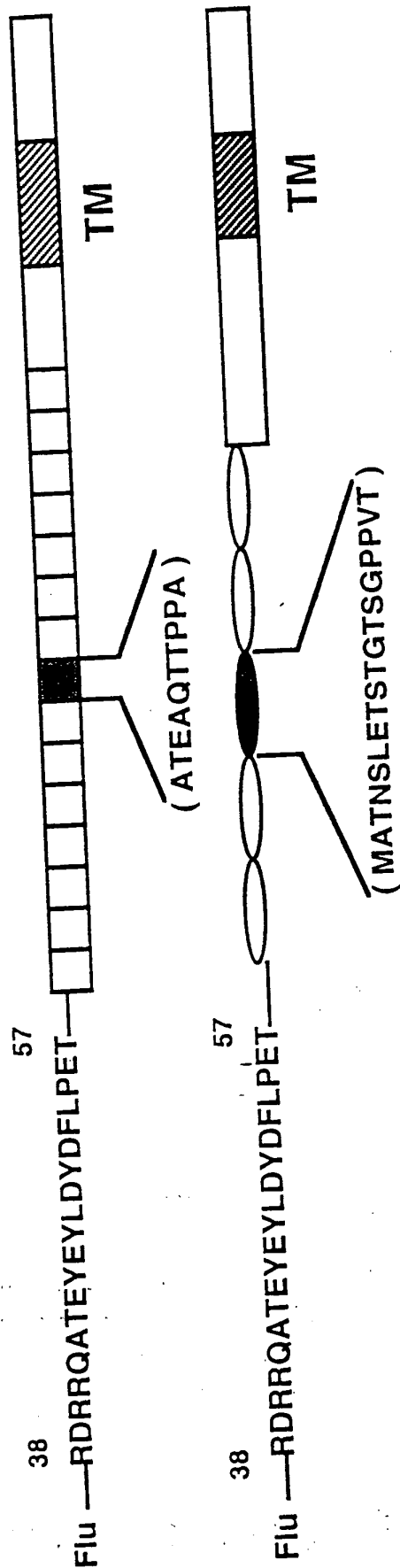
Flu —RDRRQATEYEYLDYDFLPET—

57

38

(ATEAQTTPPA)

TM

Flu —RDRRQATEYEYLDYDFLPET—

57

38

TM

(MATNSLETSTGTSGPPVT)

Construct		Binding	Expression (MFI)
FL-PSGL-1			
1R1 —RDRRQATEYEYLDYDFLPET— PSGL-1		+ + +	4.8
1R1-WT —RDRRQATEFEFLDFDFLPET— PSGL-1		+ + +	4.5
1R1-Y/F —RDRRQAAEYEYLDYDFLPEA— PSGL-1		– – –	4.5
1R1-T/A —RDRRQAAEFEFLDFDFLPEA— PSGL-1		– – –	5.8
1R1-Y/F/T/A		– – –	4.3
CD43-WT —RDRRQATEYEYLDYDFLPET— CD43		+ + +	3.1
CD43-Y/F —RDRRQATEFEFLDFDFLPET— CD43		– – –	3.0
CD43-T/A —RDRRQAAEYEYLDYDFLPEA— CD43		– – –	3.7
CD43-Y/F/T/A —RDRRQAAEFEFLDFDFLPEA— CD43		– – –	3.3

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P-Selectin Binding to COS M6 Cells Expressing Wild-Type and Mutant 20 aa Binding Domain

FIG. 10   Page 1 of 7

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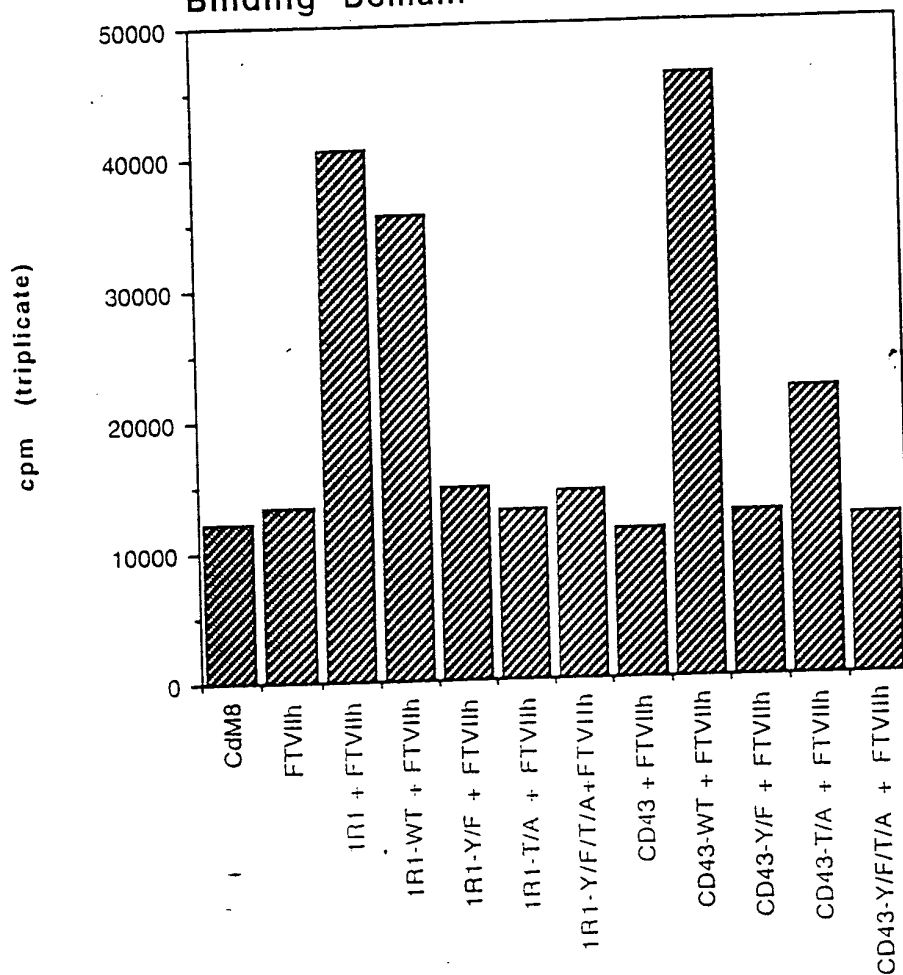
```
   AAGCTTACCACCATGGACTGGACCTGGAGGTTCCTCTTCTTTGTGGTGGCAGCAGCTACA
   ------------------------------------------------------------ 60
   TTCGAATGGTGGTACCTTGACCTTCAAGGAGAAGAAACACCACCGTCGTCGATGT
    K  L  T  T  M  D  W  T  W  R  F  L  F  F  V  V  A  A  A  T  -
```

```
61 GTGTCCAGTCCCAGGTTCAGCTCGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCC
   ------------------------------------------------------------ 120
   CCACAGGTCAGGGTCCAAGTCGACCACGTCAGACCCCGACTCCACTTCTTCGGACCCAGG
    G  V  Q  S  Q  V  Q  L  V  Q  S  G  A  E  V  K  K  P  G  S  -
```

```
121 TCGGTGAAGGTCTCCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGG
   ------------------------------------------------------------ 180
   AGCCACTTCCAGAGGACGTTCCGAAGACCTCCGTGGAAGTCGTCGATACGATAGTCGACC
    S  V  K  V  S  C  K  A  S  G  G  T  F  S  S  Y  A  I  S  W  -
```

```
181 GTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGT
   ------------------------------------------------------------ 240
   CACGCTGTCCGGGGACCTGTTCCCGAACTCACCTACCCTCCCTAGTAGGGATAGAAACCA
    V  R  Q  A  P  G  Q  G  L  E  W  M  G  G  I  I  P  I  F  G  -
```

```
241 ACAGCAAACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACG
   ------------------------------------------------------------ 300
   TGTCGTTTGATGCGTGTCTTCAAGGTCCCGTCTCAGTGCTAATGGCGCCTGCTTAGGTGC
    T  A  N  Y  A  Q  K  F  Q  G  R  V  T  I  T  A  D  E  S  T  -
```

FIG. 10   Page 2 of 08/175601

```
      AGCACAGCCTACATGAGCTTAGCAGCTTAGATCTCAGGACACTTCCCTCTATTACTCT
 301  ------------------------------------------------------------  360
      TCGTGTCGGATGTACTCGAATCGTCGGACTGTAGAGTCGTGTGCGGGACATAATGAGA
```

```
      GCGAGAGATAATGGAGCCTATTCTAGTGGTCGTAGCTCCTACTCGGGCTGGTTCGACCCC
 361  ------------------------------------------------------------  420
      CGCTCTCTATTACCTCGGATAACATCACCACCATCGACGATGAGCCCGACCAAGCTGGGG

       A  R  D  N  G  A  Y  S  G  G  G  S  C  Y  S  G  W  F  D  P  -
```

```
      TGGGGCCAGGGAACCCTGGTCACCGTCTCTTCAGGTGAGTACTGAATTCTAGCTTTCTGG
 421  ------------------------------------------------------------  480
      ACCCCGGTCCCTTGGGACCAGTGGCAGAGAAGTCCACTCATGACTTAAGATCGAAAGACC

       W  G  Q  G  T  L  V  T  V  S  S
```

```
      GGCAGGCCAGGCCTGACCTTGGCTTTGGGGCAGGGAGCGGGCTAAGGTCAGGCAGGTTGC
 481  ------------------------------------------------------------  540
      CCGTCCGGTCCGGACTGGAACCGAAACCCCGTCCCTCGCCCGATTCCAGTCCGTCCAACG
```

```
      GCCAGCAGGTGCACACCCAATGCCCATGAGCCCAGACACTGGACGCTGAACCTCGCCGAC
 541  ------------------------------------------------------------  600
      CGGTCGTCCACGTGTGGGTTACGGGTACTCGGGTCTGTGACCTGCGACTTGGAGCGGCTG
```

```
      AGTTAAGAACCCAGGGGCCTCTCGCCCTGGGCCCAGCTCTGTCCCACACCCCGGTCAGAT
 601  ------------------------------------------------------------  660
      TCAATTCTTGGGTCCCCGGAGAGCGGGACCCGGGTCGAGACAGGGTGTGGCGCCAGTCTA
```

FIG. 10   Page 3 of 7   08/756018

```
          GCACCACCTCTCTTCAGCCTTGAGCAAGGGCCCATCGTTCTTCCCCCTGGCAGGCTCC
661       --------------------------------------------------------------      720
          CCGTGGTGGAGAGAACGTCGGAGGTTCGTTCCCGGGTAGCCAGAAGGGGGACCGTCGAGG

              A   T   K   P   S   V   F   P   L   A
```

```
          TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
721       --------------------------------------------------------------      780
          AGGTTCTCGTGGAGACCCCCGTGTCGCCGGGACCCGACGGACCAGTTCCTGATGAAGGGG

          S   K   S   T   S   G   G   T   A   A   L   G   C   L   V   K   D   Y   F   P
```

```
          GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG
781       --------------------------------------------------------------      840
          CTTGGCCACTGCCACAGCACCTTGAGTCCGCGGGACTGGTCGCCGCACGTGTGGAAGGGC

          E   P   V   T   V   S   W   N   S   G   A   L   T   S   G   V   H   T   F   P
```

```
          GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC
841       --------------------------------------------------------------      900
          CGACAGGATGTCAGGAGTCCTGAGATGAGGGAGTCGTCGCACCACTGGCACGGGAGGTCG

          A   V   L   Q   S   S   G   L   Y   S   L   S   S   V   V   T   V   P   S   S
```

```
          AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG
901       --------------------------------------------------------------      960
          TCGAACCCGTGGGTCTGGATGTAGACGTTGCACTTAGTGTTCGGGTCGTTGTGGTTCCAC

          S
```

```
          GACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTGTCTGCTGGAAGCAGGCTC
961       --------------------------------------------------------------      1020
          CTGTTCTTTCAACCACTCTCCGGTCGTGTCCCTCCCTCCCACAGACGACCTTCGTCCGAG

          D   K   K   V
```

FIG. 10   Page 4 of 7

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```
      AGCGCTCCTGCCTGGACGCATCCCGGCTATGCAGCCCCAGTCCAGGGCAGCAAGGCAGGC
1021  ------------------------------------------------------------ 1080
      TCGCGAGGACGGACCTGCGTAGGGCCGATACGTCGGGGTCAGGTCCCGTCGTTCCGTCCCG


      CCCGTCTGCCTCTTCACCCGGAGCCTCTGCCCGCCCCACTCATGCTCAGGGAGAGGGTCT
1081  ------------------------------------------------------------ 1140
      GGGCAGACGGAGAAGTGGGCCTCGGAGACGGGCGGGGTGAGTACGAGTCCCTCTCCCAGA


      TCTGGCTTTTTCCCAGGCTCTGGGCAGGCACAGGCTAGGTGCCCCTAACCCAGGCCCTGC
1141  ------------------------------------------------------------ 1200
      AGACCGAAAAAGGGTCCGAGACCCGTCCGTGTCCGATCCACGGGGATTGGGTCCGGGACG


      ACACAAAGGGGCAGGTGCTGGGCTCAGACCTGCCAAGAGCCATATCCGGGAGGACCCTGC
1201  ------------------------------------------------------------ 1260
      TGTGTTTCCCCGTCCACGACCCGAGTCTGGACGGTTCTCGGTATAGGCCCTCCTGGGACG


      CCCTGACCTAAGCCCACCCCAAAGGCCAAACTCTCCACTCCCTCAGCTCGGACACCTTCT
1261  ------------------------------------------------------------ 1320
      GGGACTGGATTCGGGTGGGGTTTCCGGTTTGAGAGGTGAGGGAGTCGAGCCTGTGGAAGA


      CTCCTCCCAGATTCCAGTAACTCCCAATCTTCTCTCTGCAGAGCCCAAATCTTGTGACAA
1321  ------------------------------------------------------------ 1380
      GAGGAGGGTCTAAGGTCATTGAGGGTTAGAAGAGAGACGTCTCGGGTTTAGAACACTGTT
                                                 E  P  K  S  C  D  K  -


      AACTCACACATGCCCACCGTGCCCAGGTAAGCCAGCCCAGGCCTCGCCCTCCAGCTCAAG
1381  ------------------------------------------------------------ 1440
      TTGAGTGTGTACGGGTGGCACGGGTCCATTCGGTCGGGTCCGGAGCGGGAGGTCGAGTTC
```

FIG. 10   Page 5 of 7

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```
      GCGGGACAGGTGCCCTAGAGTAGCCTCCATCCAGGGACAGGCCCCAGCCGGGTGCTGACA
1441  ------------------------------------------------------------ 1500
      CGCCCTGTCCACGGGATCTCATCGGACGTAGGTCCCTGTCCGGGGTCGGCCCACGACTGT
```

```
      CGTCCACCTCCATCTCTTCCTCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCT
1501  ------------------------------------------------------------ 1560
      GCAGGTGGAGGTAGAGAAGGAGTCGTGGACTTGAGGACCCCCCTGGCAGTCAGAAGGAGA

                              A  P  E  L  L  G  G  P  S  V  F  L  F -
```

```
      TCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGG
1561  ------------------------------------------------------------ 1620
      AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACC

       P  P  K  P  K  D  T  L  M  I  S  R  T  P  E  V  T  C  V  V -
```

```
      TGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG
1621  ------------------------------------------------------------ 1680
      ACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACC

       - V  D  V  S  H  E  D  P  E  V  K  F  N  W  Y  V  D  G  V  E -
                                      N     S
                                      274               281
                                      (top)             (bot)
```

```
      AGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGGGTGG
1681  ------------------------------------------------------------ 1740
      TCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCCCACC

       V  H  N  A  K  T  K  P  R  E  E  Q  Y  N  S  T  Y  R  V  V -
                    N                      N     S
                                    292     295   297
                                                 (top)
```

```
      TCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGG
1741  ------------------------------------------------------------
      AGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCC  1800

  C        S  V  L  T  V  L  H  Q  D  W  L  N  G  K  E  Y  K  C  K  V  -
                                              •     •     •
                                             318   320   322


      TCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGTGGGA
1801  ------------------------------------------------------------
      AGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCACCCT  1860

           S  N  K  A  L  P  A  P  I  E  K  T  I  S  K  A  K
                                •     •     •     •
                               331   333   335   337


      CCCGTGGGGTGCGAGGGCCACATGGACAGAGGCCGGCTCGGCCCACCCTCTGCCCTGAGA
1861  ------------------------------------------------------------
      GGGCACCCCACGCTCCCGGTGTACCTGTCTCCGGCCGAGCCGGGTGGGAGACGGGACTCT  1920


      GTGACCGCTGTACCAACCTCTGTCCTACAGGGCAGCCCCGAGAACCACAGGTGTACACCC
1921  ------------------------------------------------------------
      CACTGGCGACATGGTTGGAGACAGGATGTCCCGTCGGGGCTCTTGGTGTCCACATGTGGG  1980

  C        -                         G  Q  P  R  E  P  Q  V  Y  T  L -


      TGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
1981  ------------------------------------------------------------
      ACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTC  2040

  C        P  P  S  R  D  E  L  T  K  N  Q  V  S  L  T  C  L  V  K  G -


      GCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACT
2041  ------------------------------------------------------------
                                                                   2100
```

FIG. 10   Page 7 of 7

```
      CGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTCGTCA

C         F  Y  P  S  D  L  A  V  E  W  E  S  N  G  Q  P  E  N  N  Y -


      ACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCA
2101  ------------------------------+----------------------------+  2160
      TGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGT

C         K  T  T  P  P  V  L  D  S  D  G  S  F  F  L  Y  S  K  L  T -


      CCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGG
2161  ------------------------------+----------------------------+  2220
      GGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCC

C         V  D  K  S  R  W  Q  Q  G  N  V  F  S  C  S  V  M  H  E  A -


      CTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTGCGAC
2221  ------------------------------+----------------------------+  2280
      GAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTACTCACGCTG

C         L  H  N  H  Y  T  Q  K  S  L  S  L  S  P  G  K  *


         GGCCGGC
2281     -------
         CCGGCCG
```

FIG. 11 A   Page I

```
   1  ATGGCGCTGT  CCTGGGTTCT  TACAGTCCTG  AGCCTCCTAC  CTCTGCTGGA

  51  AGCCCAGATC  CCATTGTGTG  CCAACCTAGT  ACCGGTGCCC  ATCACCAACG

 101  CCACCCTGGA  CCAGATCACT  GGCAAGTGGT  TTTATATCGC  ATCGGCCTTT

 151  CGAAACGAGG  AGTACAATAA  GTCGGTTCAG  GAGATCCAAG ·CAACCTTCTT

 201  TTACTTCACC  CCCAACAAGA  CAGAGGACAC  GATCTTTCTC  AGAGAGTACC

 251  AGACCCGACA  GGACCAGTGC  ATCTATAACA  CCACCTACCT  GAATGTCCAG

 301  CGGGAAAATG  GGACCATCTC  CAGATACGTG  GGAGGCCAAG  AGCATTTCGC

 351  TCACTTGCTG  ATCCTCAGGG  ACACCAAGAC  CTACATGCTT  GCTTTTGACG

 401  TGAACGATGA  GAAGAACTGG  GGGCTGTCTG  TCTATGCTGA  CAAGCCAGAG

 451  ACGACCAAGG  AGCAACTGGG  AGAGTTCTAC  GAAGCTCTCG  ACTGCTTGCG

 501  CATTCCCAAG  TCAGATGTCG  TGTACACCGA  TTGGAAAAAG  GATAAGTGTG

 551  AGCCACTGGA  GAAGCAGCAC  GAGAAGGAGA  GGAAACAGGA  GGAGGGGGAA

 601  TCGGATCCCG  AGGGTGAGTA  CTAAGCTTCA  GCGCTCCTGC  CTGGACGCAT

 651  CCCGGCTATG  CAGCCCCAGT  CCAGGGCAGC  AAGGCAGGCC  CCGTCTGCCT

 701  CTTCACCCGG  AGCCTCTGCC  CGCCCCACTC  ATGCTCAGGG  AGAGGGTCTT

 751  CTGGCTTTTT  CCCAGGCTCT  GGGCAGGCAC  AGGCTAGGTG  CCCCTAACCC

 801  AGGCCCTGCA  CACAAAGGGG  CAGGTGCTGG  GCTCAGACCT  GCCAAGAGCC

 851  ATATCCGGGA  GGACCCTGCC  CCTGACCTAA  GCCCACCCCA  AAGGCCAAAC

 901  TCTCCACTCC  CTCAGCTCGG  ACACCTTCTC  TCCTCCCAGA  TTCCAGTAAC

 951  TCCCAATCTT  CTCTCTGCAG  AGCCCAAATC  TTGTGACAAA  ACTCACACAT

1001  GCCCACCGTG  CCCAGGTAAG  CCAGCCCAGG  CCTCGCCCTC  CAGCTCAAGG

1051  CGGGACAGGT  GCCCTAGAGT  AGCCTGCATC  CAGGGACAGG  CCCCAGCCGG

1101  GTGCTGACAC  GTCCACCTCC  ATCTCTTCCT  CAGCACCTGA  ACTCCTGGGG

1151  GGACCGTCAG  TCTTCCTCTT  CCCCCCAAAA  CCCAAGGACA  CCCTCATGAT
```

FIG. 11 A

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```
1201  CTCCCGGACC   ●GAGGTCA  CATGCGTGGT  GGTGC●TG  AGCCACGAAG

1251  -ACCCTGAGGT  CAAGTTCAAC  TGGTACGTGG  ACGGCGTGGA .GGTGCATAAT

1301  GCCAAGACAA  AGCCGCGGGA  GGAGCAGTAC  AACAGCACGT  ACCGGGTGGT

1351  CAGCGTCCTC  ACCGTCCTGC  ACCAGGACTG  GCTGAATGGC  AAGGAGTACA

1401  AGTGCAAGGT  CTCCAACAAA  GCCCTCCCAG  CCCCCATCGA  GAAAACCATC

1451  TCCAAAGCCA  AAGGTGGGAC  CCGTGGGGTG  CGAGGGCCAC  ATGGACAGAG

1501  GCCGGCTCGG  CCCACCCTCT  GCCCTGAGAG  TGACCGCTGT  ACCAACCTCT

1551  GTCCTACAGG  GCAGCCCCGA  GAACCACAGG  TGTACACCCT  GCCCCCATCC

1601  CGGGATGAGC  TGACCAAGAA  CCAGGTCAGC  CTGACCTGCC  TGGTCAAAGG

1651  CTTCTATCCC  AGCGACATCG  CCGTGGAGTG  GGAGAGCAAT  GGGCAGCCGG

1701  AGAACAACTA  CAAGACCACG  CCTCCCGTGC  TGGACTCCGA  CGGCTCCTTC

1751  TTCCTCTACA  GCAAGCTCAC  CGTGGACAAG  AGCAGGTGGC  AGCAGGGGAA

1801  CGTCTTCTCA  TGCTCCGTGA  TGCATGAGGC  TCTGCACAAC  CACTACACGC

1851  AGAAGAGCCT  CTCCCTGTCT  CCGGGTAAAT  GAGTGCGACG  GCCG
```

FIG. 11 B

```
  1   MALSWVLTVL SLLPLLEAQI PLCANLVPVP ITNATLDQIT GKWFYIASAF

 51   RNEEYNKSVQ EIQATFFYFT PNKTEDTIFL REYQTRQDQC IYNTTYLNVQ

101   RENGTISRYV GGQEHFAHLL ILRDTKTYML AFDVNDEKNW GLSVYADKPE

151   TTKEQLGEFY EALDCLRIPK SDVVYTDWKK DKCEPLEKQH EKERKQEEGE

201   SDPEGEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT LMISRTPEVT

251   CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY RVVSVLTVLH

301   QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK

351   NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL

401   TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGK*
```
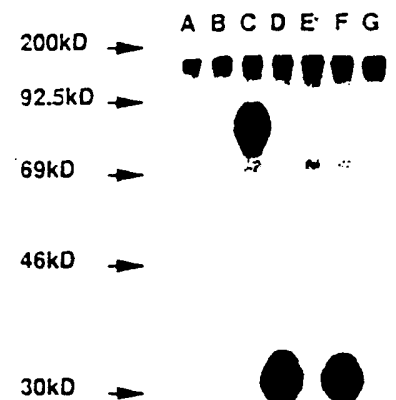
Construct

WT-hIgG   RDRRQATEYEYLDYDFLPET   [H]   [CH2]   [CH3]

Y/F-hIgG   RDRRQATEFEFLDFDFLPET   [H]   [CH2]   [CH3]

T/A-hIgG   RDRRQAAEYEYLDYDFLPEA   [H]   [CH2]   [CH3]

Y/F-T/A-hIgG   RDRRQAAEFEFLDFDFLPEA   [H]   [CH2]   [CH3]

FIG. 12A

        A B C D E F
200kD →
92.5kD →

69kD →

46kD →

30kD →

FIG. 12B

        A B C D E F G
200kD →
92.5kD →

69kD →
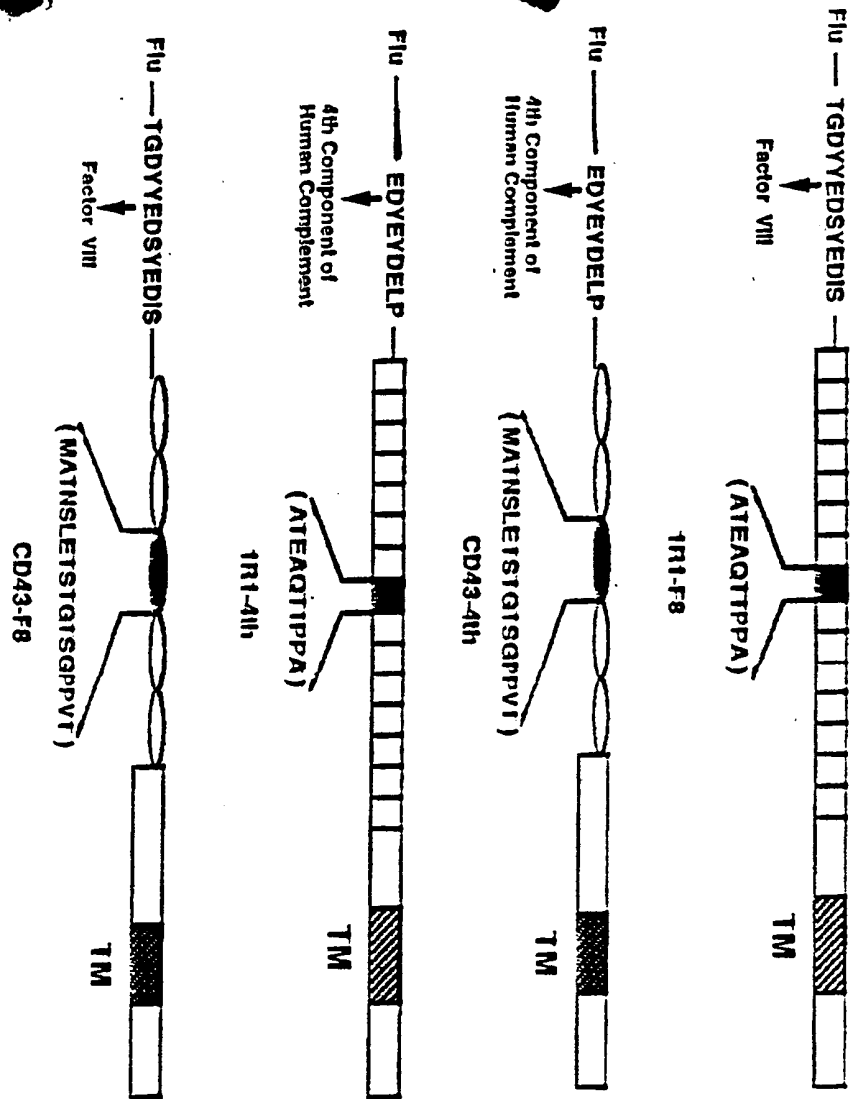
46kD →

30kD →
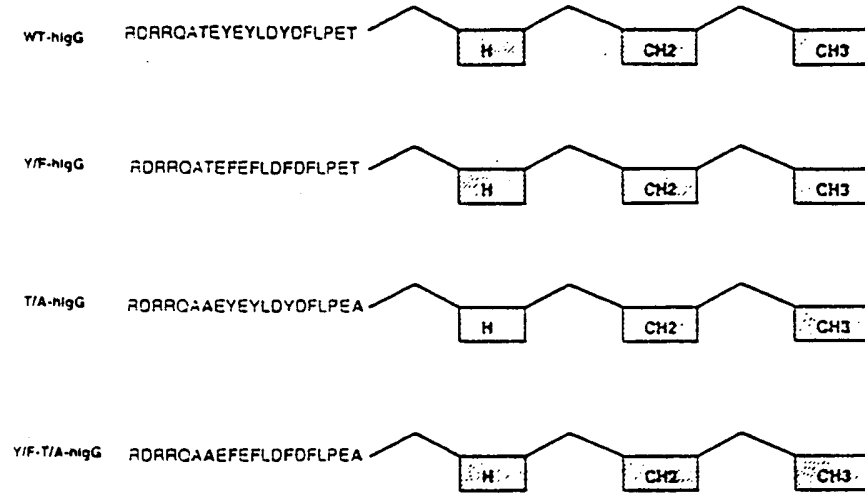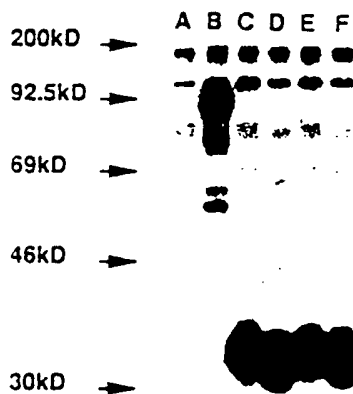
FIG. 12C
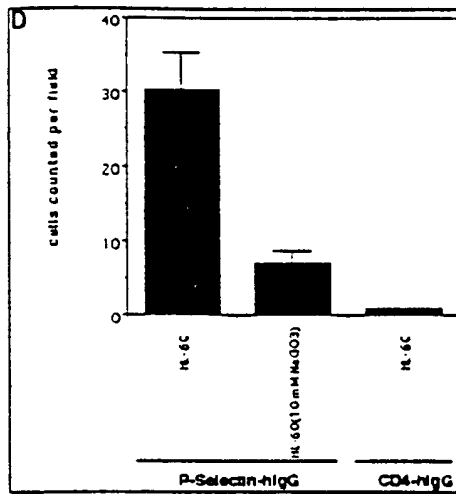
FIG. 13

FIG. 14

**P-Selectin Binding to COS M6 Cells
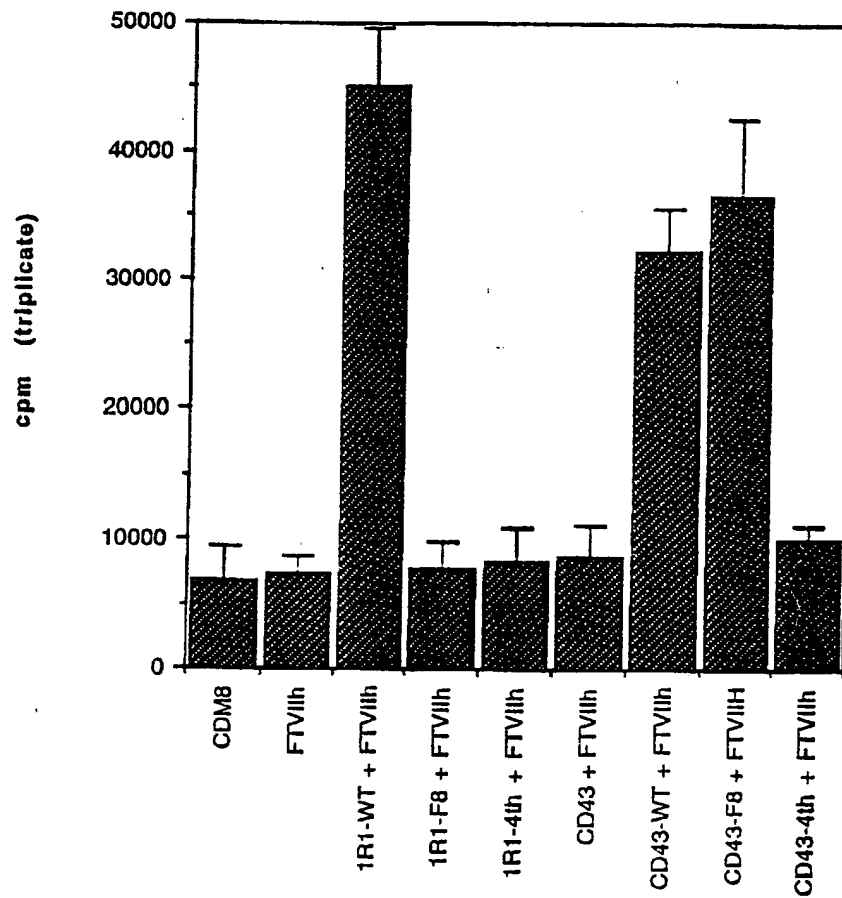Expressing Artificial Chimeric Proteins**

FIG. 15